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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/537,897	06/07/2005	Ana Isabel Sanz Molinero	BJS-4982-5	8027

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EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

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11/30/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/537,897	SANZ MOLINERO, ANA ISABEL	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *30 August 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-42* is/are pending in the application.

4a) Of the above claim(s) *5-9,18,24-28 and 35-42* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-4,10-17,19-23 and 29-34* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *07 June 2005* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *6/7/2005*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *sequence search results (3)*.

DETAILED ACTION

1. Claims 1-42 are pending.

2. Applicant's election of Group I, in the reply filed on 8/30/2007 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Claims 5-9, 18, 24-28 and 35-42 are withdrawn from consideration for being drawn to a non-elected invention.

3. Claims 1-4, 10-17, 19-23, 29-34, including SEQ ID NO:1 encoding SEQ ID NO:2 are examined in the present office action.

Specification

4. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See for example page 16, line 15. See MPEP § 608.01.

Claim Objection

5. Claim 4 is objected to for being drawn to a non-elected invention. Correction is requested.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 10-17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 10 is indefinite for reciting "the nucleic acid is as represented by SEQ ID NO:2". The Office contends SEQ ID NO:2 is an amino acid sequence so it is unclear how an amino acid sequence can be represented by a nucleic acid sequence.

Written Description

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 1-4, 10-17, 19-23 and 29-34 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to methods comprising a nucleic acid sequence encoding a 2x2CH2 zinc finger protein, or wherein said protein is from the family Brassicaceae, or from Arabidopsis, or the nucleic acid is as represented by SEQ ID NO:2 or a homologue, derivative or active fragment thereof, or wherein said nucleic acid is as represented by SEQ ID NO:1 or a portion thereof or sequences capable of hybridizing therewith, or wherein said homologue, derivative or

active fragment has any of the percent identities listed in claim 11, or wherein said nucleic acid is an alternative splice variant, or allelic variant; or a plant obtained by said method.

Because Applicants do not define the term "represent", the Office defines the term according to the Merriam Webster Online Dictionary, which defines "represent" to mean: to serve as a specimen, example or instance of, (Merriam Webster Online Dictionary. 2005, www.m-w.com/home.html; a copy of the definition is enclosed). Because Applicants define the protein and nucleic acid as being "represented" by SEQ ID NO:2 and 1, respectively, the office interprets this to read on more than just a single protein or nucleic acid sequence.

Applicants disclose SEQ ID NO:1 and SEQ ID NO:2 in the sequence listing. The Office contends, based on an interference sequence search, SEQ ID NO:1 encodes SEQ ID NO:2 (sequence search included).

The Applicants do not identify essential regions of the protein encoded by SEQ ID NO:1, nor do Applicants describe any polynucleotide sequences that encode any 2xC2H2 zinc finger protein, or a portion of a nucleic acid sequence represented by SEQ ID NO:1 that has the same activity as the protein encoded by SEQ ID NO:1.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of

cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of polynucleotide sequences encoding a protein falling within the scope of the claimed genus of polynucleotides which encode any 2xC2H2 zinc finger protein, or homologue, derivative or active fragment thereof. Applicants only describe a single sequence of SEQ ID NO:1 encoding SEQ ID NO:2. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for the protein encoded by SEQ ID NO:1, it remains unclear what features identify an Arabidopsis protein of SEQ ID NO:2. Since the genus of said proteins has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Sequences that hybridize with SEQ ID NO:1 and which are any of the percent identities listed in claim 11 encompass naturally occurring allelic variants, mutants of the protein of SEQ ID NO:2, as well as sequences encoding proteins having no known activity, of which Applicant is not in possession. Absent of such disclosure, one skilled in the art cannot determine the genus of sequences based upon the disclosure of the sequence of SEQ ID NO:1 with any certainty or predictability. Accordingly, the specification fails to provide an adequate written description to

support the broadly claimed invention. (See Written Description guidelines published in Federal Register/Vol. 66, No.4/Friday, January 5, 2001/Notices: p.1099-1111).

Scope of Enablement

8. Claims 1-4, 10-17, 19-23 and 29-34 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a method for increasing plant yield, method for increasing leaf surface area, method for prolonging vegetative growth phase and method for the production of a transgenic plant having increased yield comprising transforming a plant with a construct comprising a constitutive promoter operably linked to SEQ ID NO:1 encoding SEQ ID NO:2, does not reasonably provide enablement for said methods comprising any sequence encoding a protein exhibiting less than 100% sequence identity to SEQ ID NO:2, or any method of modifying expression of a nucleic acid sequence encoding a 2xC2H2 zinc finger by recombinant means . The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior

art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

The claims are drawn to a method for increasing plant yield, method for increasing leaf surface area, method for prolonging vegetative growth phase and method for the production of a transgenic plant having increased yield comprising a nucleic acid sequence encoding a 2x2CH2 zinc finger protein, or wherein said protein is from the family Brassicaceae, or from Arabidopsis, or the nucleic acid is as represented by SEQ ID NO:2 or a homologue, derivative or active fragment thereof, or wherein said nucleic acid is as represented by SEQ ID NO:1 or a portion thereof or sequences capable of hybridizing therewith, or wherein said homologue, derivative or active fragment has any of the percent identities listed in claim 11, or wherein said nucleic acid is an alternative splice variant, or allelic variant; or a plant obtained by said method.

Because Applicants do not define the term "represent", the Office defines the term according to the Merriam Webster Online Dictionary, which defines "represent" to mean: to serve as a specimen, example or instance of, (Merriam Webster Online Dictionary. 2005, www.m-w.com/home.html; a copy of the definition is enclosed). Because Applicants define the protein and nucleic acid as being "represented" by SEQ ID NO:2 and 1, respectively, the office interprets this to read on more than just a single protein or nucleic acid sequence.

Applicants state "A gene encoding an STZ protein was amplified by PCR from Arabidopsis thaliana seedling cDNA library" (page 35, lines 32-33), but Applicants do not disclose the primers or reaction conditions used to isolate said nucleic acid. Applicants disclose said nucleic acid was operably linked to the rice GOS2 constitutive promoter and transformed into rice (page 36, lines 14-23). Applicants disclose the resultant T1 or T2 generations

containing at least one copy of the nucleic acid exhibited increased biomass (page 38, line 19), increased above ground area of the plant (page 38, line 22), more filled seeds (page 40, lines 5-7), increased seed weight (page 40, lines 20-22), increased number of seeds per plant (page 42, lines 14-end of the page), increased root growth (page 44, lines 1-19) and increased leaf width (page 44, lines 21-34).

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that are fragments of nucleic acids or portions of nucleic acids capable of hybridizing to SEQ ID NO:1 will encode a protein with the same activity as a protein encoded by SEQ ID NO:1. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Applicant has not provided examples or guidance for selecting a sequence out of the multitude of sequences that are encompassed by Applicant's broad claim language, that gives the expected results when transformed into a plant. Transforming plants with heterologous genes that are involved in plant development produce unpredictable results. Kano-Murakami et al (1993, FEBS 334:365-368) teach introducing the *Oryza sativa* homeobox 1 (OSH1) gene into

tobacco. OSH1 is a rice homologue of the *Knotted-1* homeobox gene from maize and would be encompassed by Applicant's broad claim language. Kano-Murakami et al teach transgenic tobacco plants comprising the OSH1 gene display a "range of phenotypes which include abnormalities in leaf and petal shape as well as stem height and number" (page 365, right column, 1st paragraph).

The state-of-the-art teach that not all MYB transcription factors have the same activity and produce the same result when transformed into a plant. Payne et al (1999, Development 126:671-682) teach the *MIXTA* myb class gene from *Antirrhinum* and *CotMYBA*, a closely related MYB-class gene from cotton, was unable to replace the trichome-initiating function of the *Arabidopsis GL1* myb gene. They also teach that overexpression of *MIXTA* in *Nicotiana tabacum* resulted in the production of supernumerary trichomes whereas overexpression of *MIXTA* in *Arabidopsis* did not have the same effect (page 672, right column, 2nd paragraph) indicating that the functionality of MYB proteins is species specific.

Applicants' claims are drawn to "modifying" expression or level and/or activity of a protein but Applicants are only enabled for increasing expression or level and/or activity of a protein using recombinant DNA technology. Applicants have not shown by way of disclosure or example, that decreasing the expression or level and/or activity of a protein will result in the same phenotypes as disclosed in the specification, as discussed above. In addition, Applicants have only disclosed increasing expression by over-expressing the STZ nucleic acid molecule of SEQ ID NO:1. Applicants have not disclosed other methods of increasing expression which result in the same rice phenotypes.

Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims. Applicants have not taught which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences, either by using non-disclosed fragments of SEQ ID NO:1 as probes or by designing primers to undisclosed regions of SEQ ID NO:2 and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, in order to identify those, if any, that when over-expressed produce a plant exhibiting increased yield, increased leaf surface area and increased vegetative state, when compared to a non-transformed plant.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Claim Rejections - 35 USC § 102

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

9. Claims 1-4, 10-17, 19-23 and 29-34 are rejected under 35 U.S.C. 102(b) as being anticipated by Pineda et al (2001, WO 01/36598 A1).

The claims are drawn to a method for increasing plant yield, method for increasing leaf surface area, method for prolonging vegetative growth phase comprising modifying expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zing finger, wherein said modifying

expression is effected by recombinant means, wherein said 2xC2H2 zinc finger protein is derived from Arabidopsis thaliana, or wherein the nucleic acid is as represented by SEQ ID NO:2, or homologue, derivative or active fragment thereof, or wherein said nucleic acid is as represented by SEQ ID NO:1 or a portion thereof or sequences that hybridize therewith, or wherein said homologue, derivative or active fragment has a percent identity as recited in claim 11, or wherein said plant is a monocot, or wherein said modifying expression is effected by introducing a nucleic acid into a plant, or wherein said nucleic acid encodes a 2xC2H2 protein, or wherein said nucleic acid is an alternative splice variant, allelic variant or part of a chromosome, or wherein said modifying expression comprises increased expression, wherein expression is driven by a promoter, wherein said increased yield comprises increased above ground biomass, increased seed yield or increased root yield, or method for the production of a transgenic plant having increased yield comprising a nucleic acid sequence encoding a 2xC2H2 zinc finger protein; or a plant obtained by said method.

Because Applicants do not define the term "represent", the Office defines the term according to the Merriam Webster Online Dictionary, which defines "represent" to mean: to serve as a specimen, example or instance of, (Merriam Webster Online Dictionary. 2005, www.m-w.com/home.html; a copy of the definition is enclosed). Because Applicants define the protein and nucleic acid as being "represented" by SEQ ID NO:2 and 1, respectively, the office interprets this to read on more than just a single protein or nucleic acid sequence.

Pineda et al disclose a nucleic acid sequence having 100% sequence identity to Applicants' SEQ ID NO:1 and they disclose a nucleic acid molecule that encodes an amino acid sequence having 100% sequence identity with Applicants' SEQ ID NO:2 (sequence search

results included). Pineda et al state "The present sequence is a cDNA encoding Arabidopsis thaliana transcription factor. This novel transcription factor is useful for modifying a plant's phenotype in desirable ways, such as modifying a plants environmental stress" (see printout for ID AD06454, first page, bottom paragraph). Pineda et al disclose that the transcription factor can be used to modify the structure and developmental characteristics of plants. Pineda et al disclose a method for producing a plant having a modified environmental stress tolerance comprising altering the expression of said nucleic acid molecule, or wherein the activity of the encoded polypeptide is also modified (claim 13). Pineda et al disclose a plant comprising altered expression levels of the nucleic acid molecule (claims 25 and 26). The Office contends that the disclosed sequence of Pineda et al encompasses Applicants' claims drawn to homologues, derivatives or active fragments thereof and portions and sequences capable of hybridizing therewith. The Office contends that the methods and plants anticipate Applicants' invention because the starting materials and method steps are the same. See *Integra LifeSciences I Ltd. V. Merck KGaA* 50 USPQ2d 1846, 1850 (DC SCalif 1999), which teaches that where the prior art teaches all of the required steps to practice the claimed method and no additional manipulation is required to produce the claimed result, then the prior art anticipates the claimed method.
The Office contends claims 30-34 are drawn to plants comprising the nucleic acid sequence of Applicants, which read on the plants of Pineda et al. "[T]he discovery of a previously unappreciated property of a prior art composition, or of a scientific explanation for the prior art's functioning, does not render the old composition patentably new to the discoverer." *Atlas Powder Co. v. Ireco Inc.*, 190 F.3d 1342, 1347, 51 USPQ2d 1943, 1947 (Fed.Cir. 1999). Thus the claiming of a new use, new function or unknown property which is inherently present in the

prior art does not necessarily make the claim patentable. Therefore, Pineda et al anticipate the claimed invention.

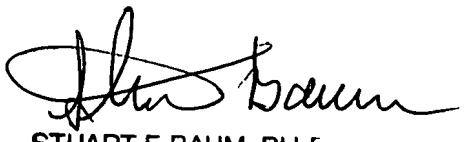
10. No claims are allowed.

11. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached at 571-272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



STUART F BAUM, PH.D
PRIMARY EXAMINER

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Art Unit 1638
November 19, 2007